



## SEQUENCE LISTING

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<110> Wilkins, Thea A.  
The Regents of the University of California

<120> Cotton Transcription Factors and Their Uses

<130> 023070-095600US

<140> US 09/453,387

<141> 1999-12-02

<160> 26

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Gossypium hirsutum

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<221> CDS

<222> (59)..(943)

<223> GhMYB1

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Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
   1               5               10               15

tgg acc aaa gag gaa gat caa cgc ctc atc aac tac atc cgt gtc cat      154
Trp Thr Lys Glu Glu Asp Gln Arg Leu Ile Asn Tyr Ile Arg Val His
               20               25               30

ggt gaa ggc tgc tgg cgt tcc ctc ccc aaa gct gct ggg ctg ctt aga      202
Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
               35               40               45

tgt ggt aag agt tgc aga tta aga tgg ata aac tac ttg agg cct gat      250
Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
               50               55               60

ctt aag aga gga aat ttc act gaa gaa gaa gat gag ctt atc atc aag      298
Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
               65               70               75               80

ctt cac agt tta ctt gga aac aaa tgg tca ttg att gct gga aga tta      346
Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
               85               90               95

cca gga aga aca gat aat gag ata aag aac tac tgg aac aca cac atc      394
Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
               100               105               110

aaa aga aag ctt ata agc aga gga att gat cca caa act cat cgt cct      442
Lys Arg Lys Leu Ile Ser Arg Gly Ile Asp Pro Gln Thr His Arg Pro
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ctc aat caa acg gcc aat acc aac aca gtc aca gcc ccc acc gaa ttg 490  
 Leu Asn Gln Thr Ala Asn Thr Asn Thr Val Thr Ala Pro Thr Glu Leu  
 130 135 140

gat ttc aga aac tcg ccc aca tcc gtt tcc aaa tcc agt tcc atc aaa 538  
 Asp Phe Arg Asn Ser Pro Thr Ser Val Ser Lys Ser Ser Ser Ile Lys  
 145 150 155 160

aac ccg tct ctg gat ttc aat tac aat gaa ttt caa ttc aag tcc aac 586  
 Asn Pro Ser Leu Asp Phe Asn Tyr Asn Glu Phe Gln Phe Lys Ser Asn  
 165 170 175

aca gat tcc ctt gaa gaa ccc aac tgt aca gcc agc agt ggc atg act 634  
 Thr Asp Ser Leu Glu Glu Pro Asn Cys Thr Ala Ser Ser Gly Met Thr  
 180 185 190

aca gat gaa gag caa caa gaa cag ctg cac aag aag cag caa tac ggt 682  
 Thr Asp Glu Glu Gln Gln Glu Gln Leu His Lys Lys Gln Gln Tyr Gly  
 195 200 205

ccg agc aat ggg caa gac ata aat ttg gag ctg tcg att ggg att gtt 730  
 Pro Ser Asn Gly Gln Asp Ile Asn Leu Glu Leu Ser Ile Gly Ile Val  
 210 215 220

tca gct gac tca tct cgg gta tca aat gcc aac tcg gcc gag tcg aaa 778  
 Ser Ala Asp Ser Ser Arg Val Ser Asn Ala Asn Ser Ala Glu Ser Lys  
 225 230 235 240

cca aag gta gat aac aac aat ttc cag ttt ctt gaa caa gct atg gtg 826  
 Pro Lys Val Asp Asn Asn Asn Phe Gln Phe Leu Glu Gln Ala Met Val  
 245 250 255

gct aag gcg gta tgt ttg tgt tgg caa tta ggt ttt gga aca agt gaa 874  
 Ala Lys Ala Val Cys Leu Cys Trp Gln Leu Gly Phe Gly Thr Ser Glu  
 260 265 270

att tgt agg aac tgt caa aat tca aat tca aat ggc ttc tat agt tat 922  
 Ile Cys Arg Asn Cys Gln Asn Ser Asn Ser Asn Gly Phe Tyr Ser Tyr  
 275 280 285

tgt aga ccc ttg gat tca tag ggatcatcttt ttcttcttttc tttctgtttt 973  
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 <213> Gossypium hirsutum

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 35 40 45  
 Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp  
 50 55 60

Leu	Lys	Arg	Gly	Asn	Phe	Thr	Glu	Glu	Glu	Asp	Glu	Leu	Ile	Ile	Lys
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Leu	His	Ser	Leu	Leu	Gly	Asn	Lys	Trp	Ser	Leu	Ile	Ala	Gly	Arg	Leu
				85					90					95	
Pro	Gly	Arg	Thr	Asp	Asn	Glu	Ile	Lys	Asn	Tyr	Trp	Asn	Thr	His	Ile
			100					105					110		
Lys	Arg	Lys	Leu	Ile	Ser	Arg	Gly	Ile	Asp	Pro	Gln	Thr	His	Arg	Pro
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Leu	Asn	Gln	Thr	Ala	Asn	Thr	Asn	Thr	Val	Thr	Ala	Pro	Thr	Glu	Leu
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Asp	Phe	Arg	Asn	Ser	Pro	Thr	Ser	Val	Ser	Lys	Ser	Ser	Ser	Ile	Lys
145					150					155					160
Asn	Pro	Ser	Leu	Asp	Phe	Asn	Tyr	Asn	Glu	Phe	Gln	Phe	Lys	Ser	Asn
				165					170					175	
Thr	Asp	Ser	Leu	Glu	Glu	Pro	Asn	Cys	Thr	Ala	Ser	Ser	Gly	Met	Thr
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Thr	Asp	Glu	Glu	Gln	Gln	Glu	Gln	Leu	His	Lys	Lys	Gln	Gln	Tyr	Gly
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Ser	Ala	Asp	Ser	Ser	Arg	Val	Ser	Asn	Ala	Asn	Ser	Ala	Glu	Ser	Lys
225					230					235					240
Pro	Lys	Val	Asp	Asn	Asn	Asn	Phe	Gln	Phe	Leu	Glu	Gln	Ala	Met	Val
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Ala	Lys	Ala	Val	Cys	Leu	Cys	Trp	Gln	Leu	Gly	Phe	Gly	Thr	Ser	Glu
			260					265					270		
Ile	Cys	Arg	Asn	Cys	Gln	Asn	Ser	Asn	Ser	Asn	Gly	Phe	Tyr	Ser	Tyr
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Cys	Arg	Pro	Leu	Asp	Ser										
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<220>  
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 <222> (72)..(752)  
 <223> GhMYB6

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ttgaaactcc g atg aga aaa cct tgc tgc gat aaa caa ggc acc aac aag 110  
 Met Arg Lys Pro Cys Cys Asp Lys Gln Gly Thr Asn Lys  
 1 5 10

gga gcc tgg tcc aag caa gaa gat caa aag ctc att gat tat ata cgt 158  
 Gly Ala Trp Ser Lys Gln Glu Asp Gln Lys Leu Ile Asp Tyr Ile Arg  
 15 20 25

att cat ggt gaa ggc tgt tgg cgt tcc ctc ccc aaa gct gca ggt ttg 206  
 Ile His Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu  
 30 35 40 45

cac cgt tgc ggt aaa agt tgc agg ctg aga tgg ata aat tac tta aga 254  
 His Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg  
 50 55 60

cca gat atc aaa cgt ggt aac ttt gct caa gac gaa gag gac tta att	302
Pro Asp Ile Lys Arg Gly Asn Phe Ala Gln Asp Glu Glu Asp Leu Ile	
65 70 75	
atc aaa ctc cat gct ctc ctt ggt aac cgg tgg tca ctg ata gct ggt	350
Ile Lys Leu His Ala Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly	
80 85 90	
aga tta cca gga aga aca gat aat gaa gtg aag aac tat tgg aat tcc	398
Arg Leu Pro Gly Arg Thr Asp Asn Glu Val Lys Asn Tyr Trp Asn Ser	
95 100 105	
cat ata aag aga aag cta atg aag atg ggg atc gat cct aat aac cat	446
His Ile Lys Arg Lys Leu Met Lys Met Gly Ile Asp Pro Asn Asn His	
110 115 120 125	
aag ttg aac caa tat cct cat cat gtt ggt ccc ctt aac ccc acc acc	494
Lys Leu Asn Gln Tyr Pro His His Val Gly Pro Leu Asn Pro Thr Thr	
130 135 140	
acc aac tcc atg gat gtg gca tgt aag ctt aga gtg tgt tca aca gac	542
Thr Asn Ser Met Asp Val Ala Cys Lys Leu Arg Val Cys Ser Thr Asp	
145 150 155	
aat gat gat ggg atc tca gat gct gca agt tat ctc gaa gac gca aca	590
Asn Asp Asp Gly Ile Ser Asp Ala Ala Ser Tyr Leu Glu Asp Ala Thr	
160 165 170	
ccg ccc act ggt ata tcc aac ttg gac ctt gat ctc aca att gct ttt	638
Pro Pro Thr Gly Ile Ser Asn Leu Asp Leu Asp Leu Thr Ile Ala Phe	
175 180 185	
cct tcg agt cct atc aag aat att att gaa gaa agc cag cag aaa aca	686
Pro Ser Ser Pro Ile Lys Asn Ile Ile Glu Glu Ser Gln Gln Lys Thr	
190 195 200 205	
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Ala Ser Ile Val Thr Asn Asp Glu Glu Glu Gln Tyr Thr Val Pro Thr	
210 215 220	
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Leu Leu Leu Phe Arg	
225	
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gtattattgt gtataaattt ggtagaaaga aagatttcaa cttaagaatt aggatcaaat	962
aactgaatga atgaacgaat tgcagataag ttgttaggag gttttcaatc aacttatctg	1022
caattaattt ggtggagctg atgtaggatg atgagttcat cgtacatgaa ctgaaccttt	1082
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 <213> Gossypium hirsutum

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 Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu His Arg Cys  
 35 40 45  
 Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp Ile  
 50 55 60  
 Lys Arg Gly Asn Phe Ala Gln Asp Glu Glu Asp Leu Ile Ile Lys Leu  
 65 70 75 80  
 His Ala Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro  
 85 90 95  
 Gly Arg Thr Asp Asn Glu Val Lys Asn Tyr Trp Asn Ser His Ile Lys  
 100 105 110  
 Arg Lys Leu Met Lys Met Gly Ile Asp Pro Asn Asn His Lys Leu Asn  
 115 120 125  
 Gln Tyr Pro His His Val Gly Pro Leu Asn Pro Thr Thr Thr Asn Ser  
 130 135 140  
 Met Asp Val Ala Cys Lys Leu Arg Val Cys Ser Thr Asp Asn Asp Asp  
 145 150 155 160  
 Gly Ile Ser Asp Ala Ala Ser Tyr Leu Glu Asp Ala Thr Pro Pro Thr  
 165 170 175  
 Gly Ile Ser Asn Leu Asp Leu Asp Leu Thr Ile Ala Phe Pro Ser Ser  
 180 185 190  
 Pro Ile Lys Asn Ile Ile Glu Glu Ser Gln Gln Lys Thr Ala Ser Ile  
 195 200 205  
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 210 215 220  
 Phe Arg  
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 <223> GhMYB7

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 Met Gly Arg Ser Pro Cys Cys Ser Lys  
 1 5  
 gaa ggc ctt aac aga gga gct tgg act gct ctt gaa gac aaa att ctt 160  
 Glu Gly Leu Asn Arg Gly Ala Trp Thr Ala Leu Glu Asp Lys Ile Leu  
 10 15 20 25

aaa gat tat atc aaa gta cac ggt gaa ggt cgt tgg aga aat ctc ccc	208
Lys Asp Tyr Ile Lys Val His Gly Glu Gly Arg Trp Arg Asn Leu Pro	
30 35 40	
aaa aga gct ggt ctt aag aga tgt ggg aaa agt tgt agg ctt cgg tgg	256
Lys Arg Ala Gly Leu Lys Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp	
45 50 55	
ttg aat tat ttg aga cct gat att aaa aga ggt aac ata tca cct gac	304
Leu Asn Tyr Leu Arg Pro Asp Ile Lys Arg Gly Asn Ile Ser Pro Asp	
60 65 70	
gag gaa gag ctt atc atc aaa ctc cac aaa ctc ttg gga aac aga tgg	352
Glu Glu Glu Leu Ile Ile Lys Leu His Lys Leu Leu Gly Asn Arg Trp	
75 80 85	
tct ttg ata gct ggg agg ctt cca gga cga aca gac aat gaa ata aag	400
Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys	
90 95 100 105	
aat tac tgg aac acc aac tta agt aaa aga gtt tcc gat cgt caa aag	448
Asn Tyr Trp Asn Thr Asn Leu Ser Lys Arg Val Ser Asp Arg Gln Lys	
110 115 120	
tca ccc gcc gct cct tcg aaa aat ccc gag gcg gct cga cga gga act	496
Ser Pro Ala Ala Pro Ser Lys Asn Pro Glu Ala Ala Arg Arg Gly Thr	
125 130 135	
gct ggt aat ggc aat acc aat ggt aat ggt agt ggt agt tcc tcg aca	544
Ala Gly Asn Gly Asn Thr Asn Gly Asn Gly Ser Gly Ser Ser Thr	
140 145 150	
cac gtg gtg cgg aca agg gcg aca agg tgc tcc aag gtt ttc ata aac	592
His Val Val Arg Thr Arg Ala Thr Arg Cys Ser Lys Val Phe Ile Asn	
155 160 165	
cct cct cac tac aca caa aac aga gac cca aag cct tct tca act tgt	640
Pro Pro His Tyr Thr Gln Asn Arg Asp Pro Lys Pro Ser Ser Thr Cys	
170 175 180 185	
tca aat cat ggg gat cac cgg gaa cct aaa aca atg aat gag ttg tta	688
Ser Asn His Gly Asp His Arg Glu Pro Lys Thr Met Asn Glu Leu Leu	
190 195 200	
tta ccg ata atg tca gaa tcc gag aat gaa ggg acg acc gat cat ata	736
Leu Pro Ile Met Ser Glu Ser Glu Asn Glu Gly Thr Thr Asp His Ile	
205 210 215	
tca tcg gat ttt aca ttt gac ttc aac atg gga gag ttt tgt tta tcg	784
Ser Ser Asp Phe Thr Phe Asp Phe Asn Met Gly Glu Phe Cys Leu Ser	
220 225 230	
gat ctt ttg aat tcc gat ttc tgc gat gta aac gag ctt aat tac agc	832
Asp Leu Leu Asn Ser Asp Phe Cys Asp Val Asn Glu Leu Asn Tyr Ser	
235 240 245	
aat ggt ttt gat tcg tca ccc tca ccg gat cag cct cct atg gat ttc	880
Asn Gly Phe Asp Ser Ser Pro Ser Pro Asp Gln Pro Pro Met Asp Phe	
250 255 260 265	

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 Ser Asp Glu Met Leu Lys Glu Trp Thr Ala Ala Ala Ser Thr His Cys  
 270 275 280

tgt cac caa agt gcg gct tcc aat ctc cag tcc ttg cct cca ttt att 976  
 Cys His Gln Ser Ala Ala Ser Asn Leu Gln Ser Leu Pro Pro Phe Ile  
 285 290 295

gaa aat gga att gaa tga ccttgaaaaa ataaaagacg aaaaatattt 1024  
 Glu Asn Gly Ile Glu  
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tctcatgtaa actaaataaaa cacatcttcc atcattaaaa aaaaaaaaaa aaaaaaa 1081

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 <212> PRT  
 <213> Gossypium hirsutum

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 Gly Glu Gly Arg Trp Arg Asn Leu Pro Lys Arg Ala Gly Leu Lys Arg  
 35 40 45  
 Cys Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp  
 50 55 60  
 Ile Lys Arg Gly Asn Ile Ser Pro Asp Glu Glu Leu Ile Ile Lys  
 65 70 75 80  
 Leu His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu  
 85 90 95  
 Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr Asn Leu  
 100 105 110  
 Ser Lys Arg Val Ser Asp Arg Gln Lys Ser Pro Ala Ala Pro Ser Lys  
 115 120 125  
 Asn Pro Glu Ala Ala Arg Arg Gly Thr Ala Gly Asn Gly Asn Thr Asn  
 130 135 140  
 Gly Asn Gly Ser Gly Ser Ser Ser Thr His Val Val Arg Thr Arg Ala  
 145 150 155 160  
 Thr Arg Cys Ser Lys Val Phe Ile Asn Pro Pro His Tyr Thr Gln Asn  
 165 170 175  
 Arg Asp Pro Lys Pro Ser Ser Thr Cys Ser Asn His Gly Asp His Arg  
 180 185 190  
 Glu Pro Lys Thr Met Asn Glu Leu Leu Leu Pro Ile Met Ser Glu Ser  
 195 200 205  
 Glu Asn Glu Gly Thr Thr Asp His Ile Ser Ser Asp Phe Thr Phe Asp  
 210 215 220  
 Phe Asn Met Gly Glu Phe Cys Leu Ser Asp Leu Leu Asn Ser Asp Phe  
 225 230 235 240  
 Cys Asp Val Asn Glu Leu Asn Tyr Ser Asn Gly Phe Asp Ser Ser Pro  
 245 250 255  
 Ser Pro Asp Gln Pro Pro Met Asp Phe Ser Asp Glu Met Leu Lys Glu  
 260 265 270  
 Trp Thr Ala Ala Ala Ser Thr His Cys Cys His Gln Ser Ala Ala Ser  
 275 280 285  
 Asn Leu Gln Ser Leu Pro Pro Phe Ile Glu Asn Gly Ile Glu  
 290 295 300

[illegible]



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Asp Glu Ala Ala Thr Asp Pro Ser Pro Gly His Gly Thr Thr Thr Glu  
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Thr Thr Gly Ile Thr Val Asp Gln Ser Asn Gln Gln Glu Val Ile Asp  
160 165 170  
  
cat cgg gtc tta aac aat act act caa gaa tca atg acc agt gag agt 640  
His Arg Val Leu Asn Asn Thr Thr Gln Glu Ser Met Thr Ser Glu Ser  
175 180 185  
  
tat atc aac act ttc tgg att cct gac cat gat tat gag cta agt aca 688  
Tyr Ile Asn Thr Phe Trp Ile Pro Asp His Asp Tyr Glu Leu Ser Thr  
190 195 200  
  
ctt gcc atg att gac cat gat tat gag cta agt aca ctt gcc atg att 736  
Leu Ala Met Ile Asp His Asp Tyr Glu Leu Ser Thr Leu Ala Met Ile  
205 210 215  
  
gac cac ttc cat gaa tgt tct tct ttt cat ctt agc tag agactatggt 785  
Asp His Phe His Glu Cys Ser Ser Phe His Leu Ser  
220 225 230  
  
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<213> Gossypium hirsutum

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35 40 45  
Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Ser Pro Asn Val  
50 55 60  
Lys Lys Gly Asp Phe Ser Glu Glu Glu Glu Asp Leu Val Ile Arg Leu  
65 70 75 80  
His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Lys Arg Val Pro  
85 90 95  
Gly Arg Thr Asp Asn Gln Val Lys Asn Tyr Trp Asn Ser His Leu Arg  
100 105 110  
Lys Lys Leu Gly Ile Ile Asp Gln Asn Lys Thr Arg Ile Asp Phe Cys  
115 120 125  
Gln Ser Ser Lys Gln Val Lys Val Cys His Val Asp Glu Ala Ala Thr  
130 135 140  
Asp Pro Ser Pro Gly His Gly Thr Thr Thr Glu Thr Thr Gly Ile Thr  
145 150 155 160  
Val Asp Gln Ser Asn Gln Gln Glu Val Ile Asp His Arg Val Leu Asn  
165 170 175  
Asn Thr Thr Gln Glu Ser Met Thr Ser Glu Ser Tyr Ile Asn Thr Phe  
180 185 190

Trp Ile Pro Asp His Asp Tyr Glu Leu Ser Thr Leu Ala Met Ile Asp  
           195                          200                          205  
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<220>  
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       'universal' MYB primer

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 <222> (3)  
 <223> n = g, a, c or t

<220>  
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20

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       'universal' MYB primer

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conserved peptide coded by degenerate 'universal'  
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<212> DNA  
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primer COT105

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<210> 14  
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<212> DNA  
<213> Artificial Sequence

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primer COT106

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<210> 15  
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primer COT107

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<210> 16  
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<212> DNA  
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primer COT108

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primer COT109

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<212> DNA  
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primer COT110

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<210> 19  
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<220>  
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primer COT111

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<210> 20  
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<223> Description of Artificial Sequence:oligonucleotide  
primer COT112

<400> 20  
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<210> 21  
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<220>  
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 primer COT113

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 primer COT114

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<210> 23  
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 primer COT115

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<210> 24  
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<210> 25  
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<220>
<223> Description of Artificial Sequence:conserved motif
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      domain

<220>
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<223> Xaa = any amino acid

<400> 25
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 1             5

<210> 26
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<212> PRT
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<220>
<223> Description of Artificial Sequence:cysteine-rich
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<220>
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<222> (2)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (4)..(13)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (15)..(16)
<223> Xaa = any amino acid

<400> 26
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 1             5             10             15
Cys

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